```
ATGAGCTCCCGAATCGTCAGGGAGCTCGCCTTAGTCGTCACCCTTCTCCACTTGACCAGG
M  S  S  R  I  V  R  E  L  A  L  V  V  T  L  L  H  L  T  R

GTGGGGCTCTCCACCTGCCCCGCTGACTGCCACTGCCCCCTGGAGGCQCCCAAGTGCGCG
V  G  L  S  T  C  P  A  D  C  H  C  P  L  E  A  P  K  C  A

CCGGGAGTCGGGCTGGTCCGGGACGGCTGCGGCTGTTGTAAGGTCTGCGGCAAGCAGCTC
P  G  V  G  L  V  R  D  G  C  G  C  C  K  V  C  A  K  Q  L

AACGAGGACTGCAGAAAAACGCAGCCCTGCGACCACACCAAGGGGCTGGAATGCAACTTC
N  E  D  C  R  K  T  Q  P  C  D  H  T  K  G  L  E  C  N  F

GGCGCCAGCTCCACCGCTCTGAAGGGGATCTGCAGAGCTCAGTCAGAGGGCAGACCCTGT
G  A  S  S  T  A  L  K  G  I  C  R  A  Q  S  E  G  R  P  C

GAATATAACTCCAGAATCTACCAAAACGGGGAAAGTTTCCAGCCCAACTGTAAACATCAG
E  Y  N  S  R  I  Y  Q  N  G  E  S  F  Q  P  N  C  K  H  Q

TGCACATGTATTGGATGGCGCCGGGGGGCTTGCATTCCTCTGTGTCCCCAAGAACTATCT
C  T  C  I  G  W  R  R  G  A  C  I  P  L  C  P  Q  E  L  S

CTCCCCAACTTGGGCTGTCCCAACCCTCGGCTGGTCAAAGTTACCGGGCAGTGCTGCGAG
L  P  N  L  G  C  P  N  P  R  L  V  K  V  T  G  Q  C  C  E
```

MATCH WITH FIG. 1B

FIG. 1A

MATCH WITH FIG.1A

GAGTGGGTCTGTGACGAGGATAGTATCAAGGACCCCATGGAGGACCAGGACGGCCTCCTT
E W V C D E D S I K D P M E D Q D G L L

GGCAAGGGGCTGGGATTCGATGCCTCCGAGGTGGAGTTGACGAGAAACAATGAATTGATT
G K G L G F D A S E V E L T R N N E L I

GCAGTTGGAAAAGGCAGCTCACTGAAGCGGCTCCCTGTTTTTGGAATGGAGCCTCGCATC
A V G K G S S L K R L P V F G M E P R I

CTATACAACCCTTTACAAGGCCAGAAATGTATTGTTCAAACAACTTCATGGTCCCAGTGC
L Y N P L Q G Q K C I V Q T T S W S Q C

TCAAAGACCTGTGGAACTGGTATCTCCACACGAGTTACCAATGACAACCCTGAGTGCCGC
S K T C G T G I S T R V T N D N P E C R

CTTGTGAAAGAAACCCGGATTICTGAGGTGCGGCCTTGTGGACAGCCAGTGTACAGCAGC
L V K E T R I C E V R P C G Q P V Y S S

CTGAAAAAGGGCAAGAAATGCAGCAAGACCAAGAAATCCCCCGAACCAGTCAGGTTTACT
L K K G K K C S K T K K S P E P V R F T

MATCH WITH FIG.1C

FIG.1B

MATCH WITH FIG.1B

```
TACGCTGGATGTTTGAGTGTGAAGAAATACCGGCCCAAGTACTGCGGTTCCTGCGTGGAC
Y  A  G  C  L  S  V  K  K  Y  R  P  K  Y  C  G  S  C  V  D

GGCCGATGCTGCACGCCCCAGCTGACCAGGACTGTGAAGATGCGGTTCCCCTGCGAAGAT
G  R  C  C  T  P  Q  L  T  R  T  V  K  M  R  F  P  C  E  D

GGGGAGACATTTTCCAAGAACGTCATGATGATCCAGTCCTCCAAATGCAACTACAACTGC
G  E  T  F  S  K  N  V  M  M  I  Q  S  S  K  C  N  Y  N  C

CCGCATGCCAATGAAGCAGCGTTTCCCTTCTACAGGCTGTTCCAATGA
P  H  A  N  E  A  A  F  P  F  Y  R  L  F  Q  *
```

FIG.1C

```
  1  MSSRIVRELALVVTLLHLTRVGLSTCPADCHCPLEAPKCAPGVGLVRDGC  50
     |||...|.||:.||||||||::||||||.||||||||||||||||||||
  1  MSSSTFRTLAVAVTLLHLTRLALSTCPAACHCPLEAPKCAPGVGLVRDGC  50

 51  GCCKVCAKQLNEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC  100
     ||||||||||||||.||||||||||||||||||||||||||||||||||||
 51  GCCKVCAKQLNEDCSKTQPCDHTKGLECNFGASSTALKGICRAQSEGRPC  100

101  EYNSRIYQNGESFQPNCKHQCTCIGWRRGACIPLCPQELSLPNLGCPNPR  150
       MATCH WITH FIG.2B
```

FIG.2A

MATCH WITH FIG.2A

```
101  EYNSRIYQNGESFQPNCKHQCTCID.GAVGCIPLCPQELSLPNLGCPNPR  149

151  LVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKGLGFDASEVELTRNNELI  200
150  LVKVSGQCCEEWVCDEDSIKDSLDDQDDL....LGLDASEVELTRNNELI  195

201  AVGKGSSLKRLPVFGMEPRILYNPL..QGQKCIVQTTSWSQCSKTCGTGI  248
196  AIGKGSSLKRLPVFGTEPRVLFNPLHAHGQKCIVQTTSWSQCSKSCGTGI  245

249  STRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR  298
246  STRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPVR  295

299  FTYAGCLSVKKYRPKYCGSCVDGRCCTPQLTRTVKMRFPCEDGETFSKNV  348
296  FTYAGCSSVKKYRPKYCGSCVDGRCCTPLQTRTVKMRFRCEDGEMFSKNV  345

349  MMIQSSKCNYNCPHANEAAFPFYRLFQ                          375
346  MMIQSCKCNYNCPHPNEASFRLYSLFN                          372
```

FIG.2B

```
1    MSSRIVRELALVVTLLHL.TRVGLS.TCPADCHCPLE.APKCAPGVGLVR  47
     | ..:. .:.|.:.|| | ||.: : .|.|:|:|: | ||.|::||:||
1    MLASVAGPISLALVLLALCTRPATGQDCSAQCQCAAEAAPHCPAGVSLVL  50

48   DGCGCCKVCAKQLNEDCRKTQPCDHTKGLECNFGASSTALKGICRAQSEG  97
     ||||||:||||||.| | . :|||. ||| |:||....   |:| |. :|
51   DGCGCCRVCAKQLGELCTERDPCDPHKGLFCDFGSPANRKIGVCTAK.DG  99

98   RPCEYNSRIYQNGESFQPNCKHQCTCIGWRRGACIPLCPQELSLPNLGCP  147
      || :.:.:|..|||||..||.||||::   .:|:|||. ::.||. :||
100  APCVFGGSVYRSGESFQSSCKYQCTCLD.GAVGCVPLCSMDVRLPSPDCP  148

148  NPRLVKVTGQCCEEWVCDEDSIKDPMEDQDGLLGKGLGFDASEVELTRNN  197
      || ||:.|.||.||||||.. :.::          | ::.|  :| |
149  FPRRVKLPGKCCKEWVCDEPKDRTAV.........GPALAAYRLEDT...  186

198  ELIAVGKGSSLKRLPVFGMEPRILYNPLQGQKCIVQTTSWSQCSKTCGTG  247
                     || :| ::      ..|:||||.|||.||||| |
187  ................FGPDPTMM.....RANCLVQTTEWSACSKTCGMG  215

248  ISTRVTNDNPECRLVKETRICEVRPCGQPVYSSLKKGKKCSKTKKSPEPV  297
     |||||||||. ||| |:.|:| ||||:..: .::|||||| :|.| :.||
216  ISTRVTNDNTFCRLEKQSRLCMVRPCEADLEENIKKGKKCIRTPKIAKPV  265

298  RFTYAGCLSVKKTRPKYCGSCVDGRCCTPQLTRTVKMRFPCEDGETFSKN  347
     :|...|| |||.||:|:|| |.|||||||: | |:.: |.|.|||.:.||
266  KFELSGCTSVKTTRAKFCGVCTDGRCCTPHRTTTLPVEFKCPDGEIMKKN  315

348  VMMIQSSKCNYNCPHANE..AAFPFYRLFQ                      375
     :|:|..: |:|||| .|:  ..: : :::.
316  MMFIKTCACHYNCPGDNDIFESLYYRKMYG                      345
```

FIG.3